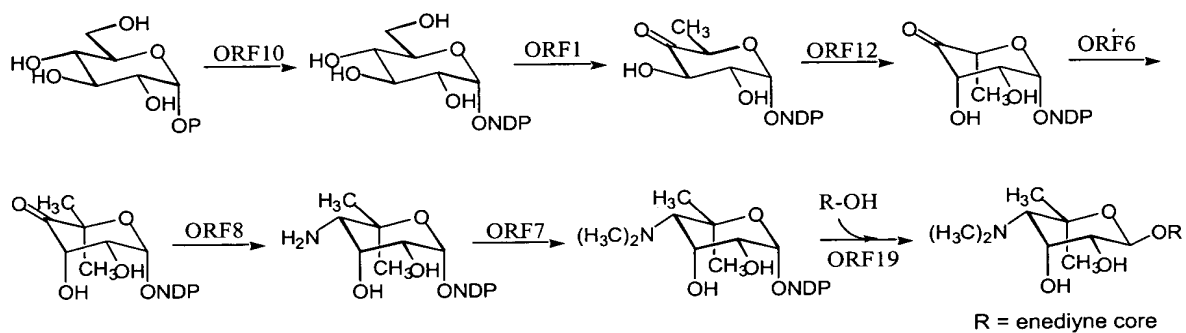


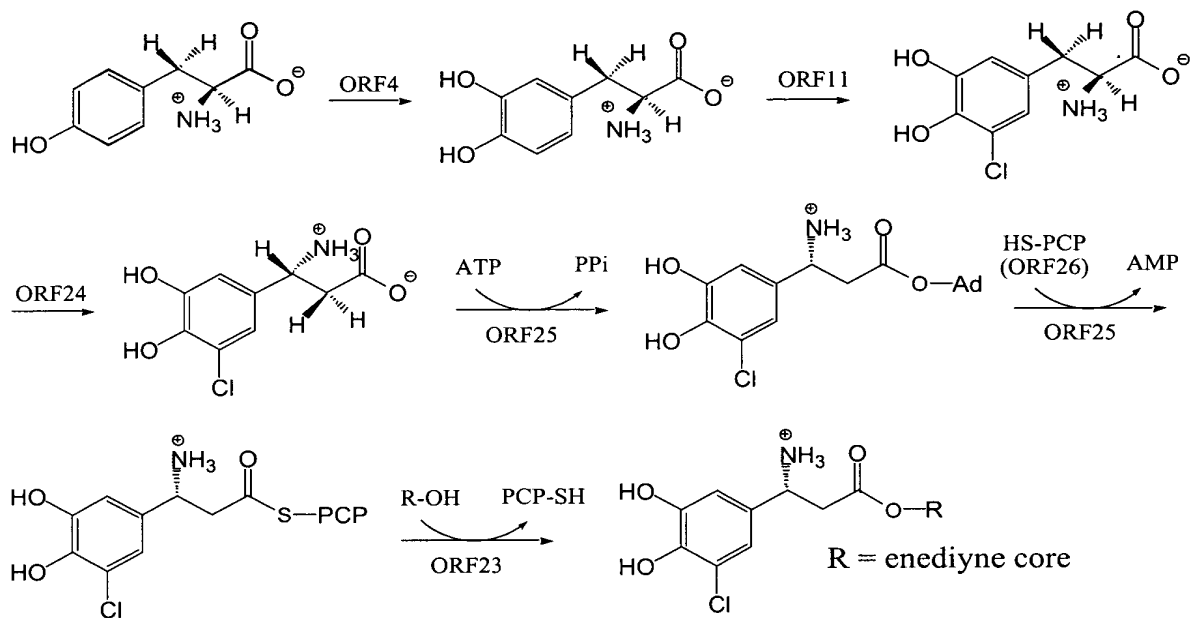
Fig. 1



ORF10: dNDP-glucose synthase, 355 aa
 ORF1: dNDP-glucose dehydratase, 332 aa
 ORF12: epimerase, 192 aa
 ORF8: aminotransferase, 410 aa

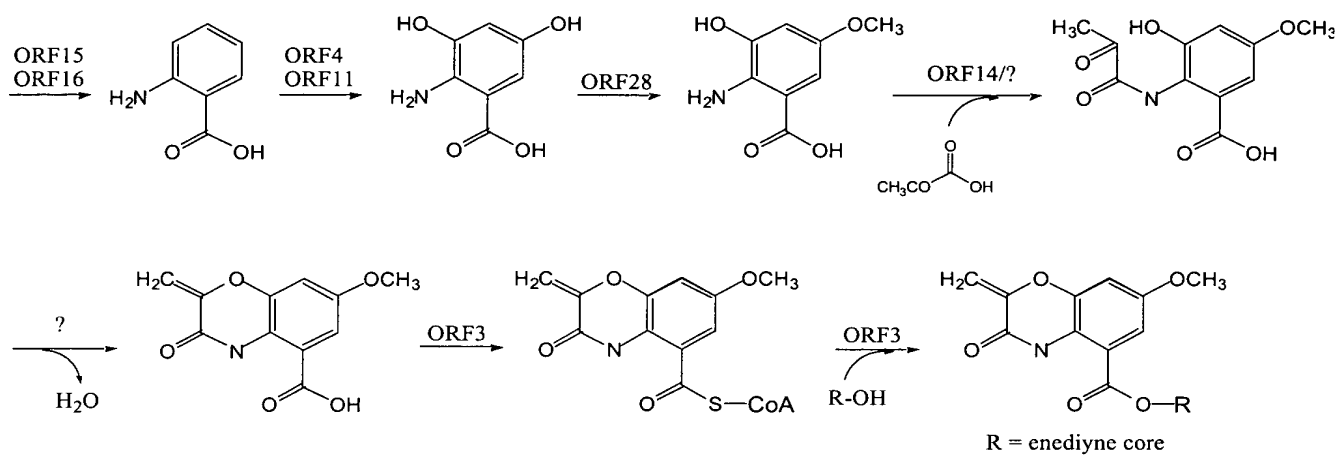
ORF6: C-methyltransferase, 423 aa
 ORF7: N-methyltransferase, 244 aa
 ORF19: glycosyl transferase, 459 aa

Fig. 2



ORF4: Hydroxylase, 527 aa ORF23: Type II NRPS condensation enzyme, 459 aa
 ORF11: Hydroxylase/halogenase, 492/494 aa ORF25: Type II NRPS adenylation enzyme, 716 aa
 ORF24: Aminomutase, 539 aa ORF26: Type II peptidyl carrier protein, 93 aa

Fig. 3A



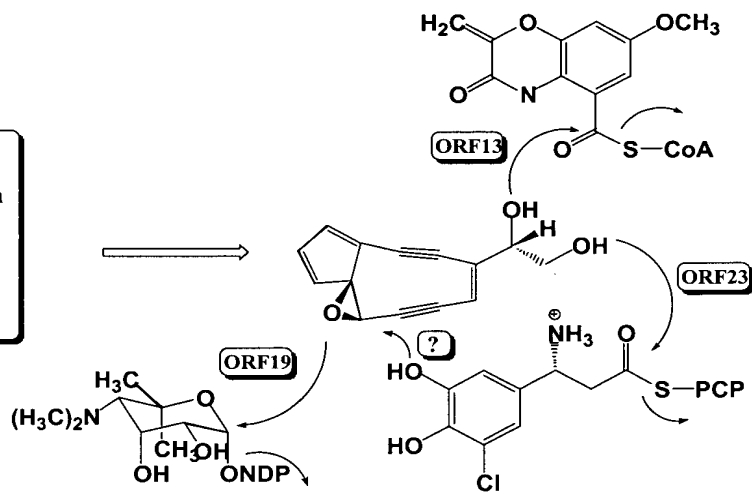
ORF15: Anthranilate synthase I, 493 aa	ORF3: Coenzyme F390 synthetase, 463 aa
ORF16: Anthranilate synthase II, 220 aa	ORF14: Coenzyme F390 synthetase, 484 aa
ORF28: O-methyltransferase, 350 aa	ORF13: O-acyltransferase, 378 aa

Fig. 3B

Fatty acid



ORF17: Epoxide hydrolase
ORF20: Monooxygenase
ORF21: Iron-sulfur flavoprotein
ORF29: P-450 hydroxylase
ORF30: Oxidoreductase
ORF32: Oxidoreductase
ORF35: Proline oxidase
ORF38: P-450 hydroxylase



ORF13: O-acyltransferase, ORF19: Glycosyl transferase, ORF23: Type II NRPS condensation enzyme

Fig. 4

Fig. 5A

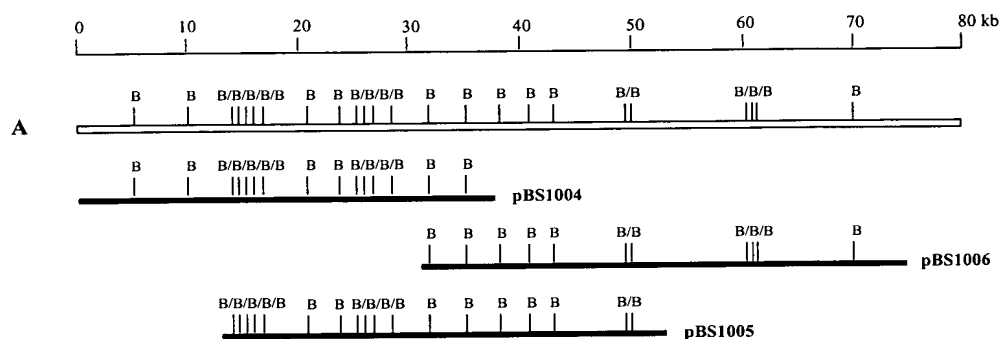


Fig. 5B

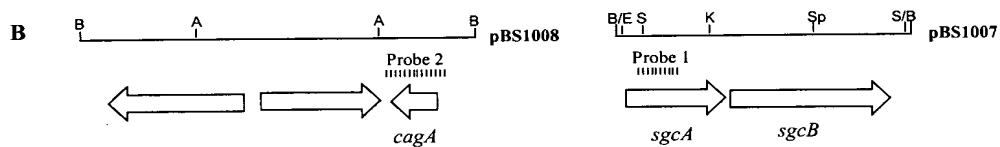


Fig. 5C

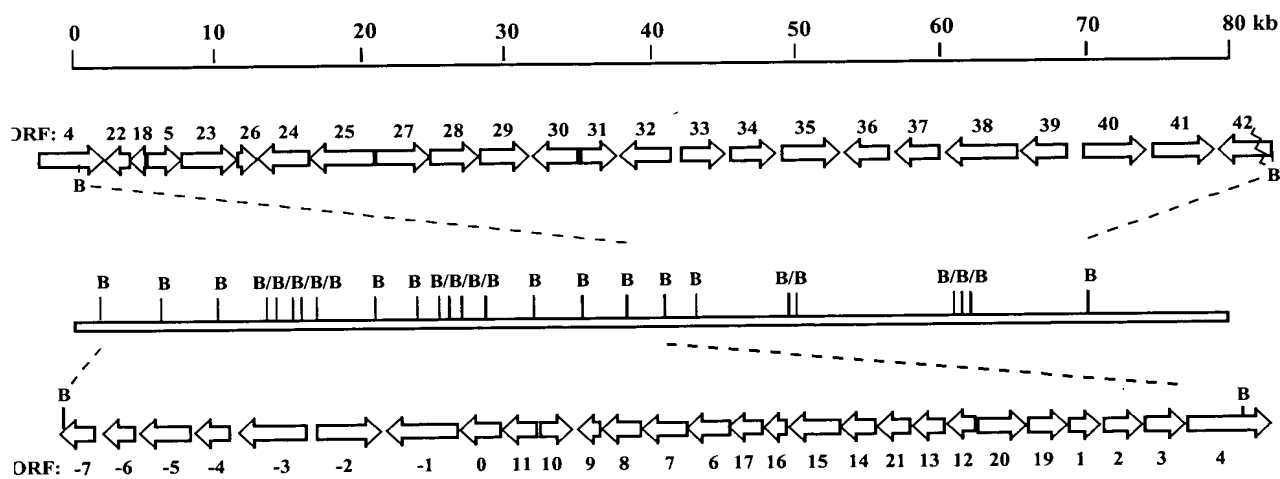


Fig. 6

1	BamHI	EcoRI	GGATCCGGGAAGACCGGAATTCGGCCCGCCAGCCCGGTGCGAACTCGTATCGTCTCTGGTAGAACTGACAAAGCGTCAATCGCCCTGACAGAGGGCGGACCG	100
101			ATGAGGATGCTGTTACGGCGGAGAGCGGGTTTCATCGGCTCGAGTTCTGTCGGGCCCACTGACGGCGAGCTCCGGGTTCCGAGGACGCCCGCGGTGA	200
			M R M L V T G G A G G F I G S Q F V R A T L H G E L P G S E D A R V T	
			SacII	
201			CGTCTCGACAAGCTGACGTPACTCCGGCAATCCGGCCAACTCACCTCGTTCGGGGCCCATCCGGGTACACCTTCGTCCAGGGCGACACCGTCGACCC	300
301			V L D K L T Y S G N P A N L T S V A A H P R Y T F V Q G D T V D P	
401			CGCGTCTGTCACGAGGTGTCGGCGCCACGACGTATCGTCCACTTCGGCGGAGTGCACGTGACCGTCTGATCGACACGCCACCGGTTCGTC	400
			R V V D E V V A G H D V I V H F A A E S H V D R S I D D T A T R F V	
501			AGAACCAACTCTCGGACCCAGACCGTCTGGAAGCGGTCTCCGGACCGGGTCGGCGGTTTCGTGCACGTTCGACCCAGCAGGTCTACGGGTCTGA	500
601			T T N V L G T Q T L L E A A L R H G V G R F V H V S T D E V Y G S I	600
701			TCGCTCCCGGCTCATGACCCGAGGACACCCCGTTCGCCCCAAAGTCCCTACGGCGGTGCAAGGGCGGTTTCGGACCTGATGGCGCTCGCCTGGCACCG	700
			A S G S W T E D T P L A P N V P Y A A S K A G S D L M A L A W H R	
801			CACCGGGCTTGAGCTCGTCAACCGGTGCACCAACACTACAGTACCCCGAGAAGGTGATCCCGCTTTCGTTCACCAACATCTCTC	800
			T R G L D V V V T R C T N N Y G P Y Q Y P L F V T N I L	
901			GACGGTTCGGGGTGCCTGTACGGGACGGCGCCACCGCGGGACTGGTGCAGTTCGACCACTGCCGGGCCATCCAGATGGTCATGAATCCCG	900
			D G G L R V P L Y G D G A H R R D W L H V S D H C R A I Q M V M N S G	
1001			GCCGGCCGGGAGGTCTACCATCGGCGGCGACACCGAACTCTCAACAGGAATCAACGGCCCTTGTCTACGGCGTCGCGCACCGACTGGTCTGTG	1000
			R A G E V Y H I G G T E L S N E E L T G L L T A C G T D W S C	
1101			CGTGACCGGTTGCCACCGCGAGGCGACGACCGCGCTACTCGTCTGACATCAGGAAGTCCGGCAGGAATCGGGTCTACGAGCCCTTGGTTCGCTTC	1100
			V D R V A D R Q G H D R R Y S L D I T K I R Q E L G Y E P L V A F	
			KpnI	
1201			GAGGACGGCTGGCCGCGACGGTGAAGTGGTATCACAGAGAACCGTTCTGTGTGGCAGCCGCTGAAGGAAGCGCGCGCTCTCTGAGACGCCCTCGGCTGAC	1200
			E D G L A A T V K W Y H E N R S W W Q P L K E A A G L L D A V G *	
1301			GGCAGCCACCGCTAGGAACACCCCAAGGAGCCACCTCCGTGACAGCACTCAAGAGCCGACGTCCTCCGCGCAGGACCGCGGGAGTGGATCGCTCTCG	1300
			SgcB > M T A V K E P T S R A G R R E W I A L V	
1401			TCGTCTCTCTCCCAAGATGCTGTGATGTGGACATCAACGCTCTCATGCTGGCCTTCGGCAGTTGACGAGGATCTCGGCGCGAGCACGCA	1400
			V L S L P T M L L M L D I N V L M L A L P Q L S E D L G A S T Q	
1501			ACAGTGTGGATCACCAGATCTACGGATTCGGGATCGCGGCTTCTGTGTGACCATGGGCACCTCCGCGCAGCCGATCGGCCCGCAGGCTCTCTGCTC	1500
			Q L W I T D I Y G F A I A G F L V T M G T L G D R I G R R L L L	
1601			GGGGCGCGGCGCTTCTCGCGGTGTCGTGTCGCCGGTTCCTCCAGACGCGCGGATGTCGTCTCAGCCGCGCGCTGCTCGGCGTCGCGCGGG	1600
			G G A A V F A V S V V A A F S D S A A M L V V S R A V L G V A G A	
1701			CCACGGTATGCCCTCGAGCTCGGCTCATCAGAACATGTCGAGGACCCCAAGAGCGGGCACCCGCATCGCCATGTGGCGCAGCCATGATGAC	1700
			T V M P S T L A L I S N M F E D P K E R G T A I A M W A S A M M A	
			CGVATCGCCCTCGGCGCGCTGCTGCTCGCGGCTTCTGTGTGGGATCGGTGTTCTCTCATCGCGCTTCGGGTGATGCTGCTGTGTTG	
			G V A I L G P A V G G L V L A A F W W G S V F L I A V P V M L L L V V	

Fig. 6 cont'd.

1701 GTCACGGGCCCGTGTCTACCGAGTCCCGGACCCGGACCGGACGGTGGACCTCTAGCGCGGGGCTCTCCCTCGCGACCGTGTGCCGTGA
 V T G P V L L T E S R D P D A G R L D L S A G L S L A T V L P V I
 1801 TCTACGACTGAAGAGTGGCCCGGACCGGGTGGACCCCGTCCGCCCGGGGTGCTCCGCGGTATCTTCGCGCGCTGTTCAGCGCCCA
 Y G L K E L A R T G W D P L A G A V V L G I F G A L F V Q R Q
 1901 GCGCGGTTGGCCGACCCCATGCTGGACCTTGGCCCTTTCGCGGACCGACCCCTCGCGGGGGTCTGACGGTCAAGCCGTCATCATGGGC
 R R L A D P M L D L G L F A D R T L R A G L T V S L V N A V I M G
 SphI
 2001 GGGACGGGACTGATGGTCCCTGTACTCCAGACATCGCCGGTCACTCCCGTTGGCCCGGGTGTGGCTGTGATCCCGGCTTCATGCTCGTCG
 G T G L M V A L Y L Q T I A G H S P L A A G L W L L I P A C M L V V
 2101 TGGCGTACAGTGTGAACTGCTGGCCAGCGGATGCCCTTCCCGGTGCTGTGGGGGACTGTATCGCGCGCTCGGACAGTCTCTGATCAC
 G V Q L S N L L A Q R M P S R V L L G G L L I A A V G Q L L I T
 2201 CCAGGTGGACACCGAGGACACCGCCCTCTCATCGGGCCACACCTGATCTACTTCGGCGCCTCACCGTGGGGCCGATCACCGGGCGCGATCATG
 Q V D T E D T A L L I A A T T L I Y F G A S P V G P I T T G A I M
 2301 GGAGCCGCCCCCGGAGAGGGGTGCCGCTCGTGTGCTGTCGCCACCGCGCGGAGTTCGAGTGGCGCTCGGCATCGCGGCGCTGGGGAGTCTGG
 G A A P E K A G A S L S A T G G E F G V A L G I A G L G S L G
 2401 GCACCGTGTGTACAGCGCGGGTTCGAGTGCAGGACGGCGGGCCCGGAGCCGCGAGCGCGGAGAGAGCATGCGCGGCGCCCTGCACACGGC
 T V V Y S A G V E V P D A A G P A D A A Q E S I A G A L H T A
 2501 CGGTCACTGGCACCGGAGCGCGACGCCCTGTGACTCCGCGCGCGCGCTTCAACAGCGCGTGCAGTCCGTCCGCGCGCTGTGCCCGCTGTTC
 G Q L A P G S A D A L L D S A R A A F T S G V Q S V A A V C A V F
 2601 TCCCTGGCGCTCGCGTCTCATCGGCACCGGCTGGGGACATTTCCGGATGGACACCGGCGAGGAAACCGCGGAGAACGACGCTCAACCGG
 S L A L A V L I G T R L R D I S A M D H G H E P A E N D A Q P A
 2701 CCACATGAGCGCACTTCCGGAGATGCAACGGCCCGCTCGAGGTATGAGATCACCTTCGGGGTGCACCTGCACGGCAACGGAGGCGTAGTGGAGTACT
 T *
 2801 GGAACAGCACGGCGGAGACCATGCCCGCCAGGAACTCGAACAGTGGCGCAGGCTCCAGGCGCGCATGGACCAACGCCAGAGGCTTTGCCCTT
 SacII
 2901 CTGGCGGGAACGACTCCCGAGAACATCACTCCATGGCGGACTACGGCGCGGGTGCCTCTCCTGCGCAAGGCGGACCTCCTCGCGCGGGAAGCCGCG
 BamHI
 3001 TCTCCCCCTTACGGCACCTGGCCCTCGCTGGATCC
 3035

Fig. 7

Gdh 1:~~~MEVLVTGGAGFIGSHYVROLLGAYPAFAGADVVLDKLTYAGNEENLRPVADDPRF: 57
 Tyla2 1:~~~MEVLVTGGAGFIGSHYVROLLGAYPDLGATRTVVLDKLTYAGNPANLEHVAGHPDL: 57
 SgcA 1:~~~MEVLVTGGAGFIGSOFVRATLHGELPESSEDARVTVLDKLTYSGNPANLTSVAAHPRY: 57
 MtmE 1:MTTTSILVTGGAGFIGSHYVRTLIGER..GVPDVTTVVLDKLTYAGTLTNLAEVSDSDRF: 58
 consensus 1: mrVLVTGGAGFIGShyvr lL g pa v VLDKLTyaGn NL Va prf: 60

Gdh 58:RFVRGDIcEWDVSEVMREVDVVVFHFAAEThVDRSILGASDFVVTNVVGTNTLLQCALAA:117
 Tyla2 58:EFVRGDIADHGWWRRRLMEGVGLVVHFAAESHVDRSIESSEAFVRTNVEGTRVLLQAAVDA:117
 SgcA 58:TFVQGDITVDPRVDEVVAGHDVVFHFAAESHVDRSIDTATRFVTTNVLGTQTLLEAALRH:117
 MtmE 59:RFVRGDIcDAPLVDDLAVHDQVVHFAAESHVDRSILGAADFVRTNVVTGTQTLDDAALRQ:118
 consensus 61: FVrGDi d vv evm dvvVFHFAAEshVDRSI a FV TNV GTntLL aAl :120

Gdh 118:NVSKFVHVSTDEVYGTIEHGSWPEDHLLTEPNSPYSAAKAGSDLIARAYHRTHGGLPVCITR:177
 Tyla2 118:GVGRFVHISTDEVYGSIAEGSWPEDEHPVAPNSPYAATKAASDLLALAYHRTYGLDVRVTR:177
 SgcA 118:GVGRFVHVSTDEVYGSIASGSWTEDTELAPNVPIAASKAGSDLMALAWHRTRGLDVVVTR:177
 MtmE 119:GIETEFVHISTDEVYGSIDAGSWPETAPVSPNSLYSAAKASSDLVALAYHRTHGGLDVRVTR:178
 consensus 121:gv kFVHVSTDEVYGSi GSWped pl PNspY A KAgSDLiAlaYHRTHGldv vTR:180

Gdh 178:CSNNYGPYQFPEKVLPLFITNLMDGRRVPLYGDGLNVRDWLHVTDHCRGIQLVAESGRAG:237
 Tyla2 178:CSNNYGPRQYPEKAVPLFITNLMDGLFVPLYGDGNTREWLHVDDHCRGVALVGAGGRPG:237
 SgcA 178:CTNNYGPYQYPEKVLPLFITNLMDGLRVPLYGDGAHRRDWLHVSDHCRATQVMVNSGRAG:237
 MtmE 179:CSNNYGSQFPEKVLPLFITNLMDGREVPLYGDGTNVRDWLHVDDHVRAIELVRTGGRAG:238
 consensus 181:CsNNYGp QfPEKvLPLFiTnlldG VPLYGDG n RdWLHV DHcRgi lv GRaG:240

Gdh 238:EIYNIGGGTELTKNELTERVLELMCQDWSMVQPVTDKRGHDDRRYSVDHTKISEELGYEPV:297
 Tyla2 238:VIYNIGGGTELTKNELTDRIELCGADRSALRRVADRPQGHDDRRYSVDHTKIREELGYAPR:297
 SgcA 238:EVYHIGGGTELSNEELTGLLLTACGTDWSCVDRVADRQGHDDRRYSLDITKIRQELGYEPL:297
 MtmE 239:EVYNIGGGTELSNKELTQLLLDACGAGWDRVRYVTDKRGHDDRRYSVDCTKIRRELGYRPA:298
 consensus 241:eiYnIGGGTELtN ELT vLe cG dws v V DR GHDDRRYSvD TKIr ELGY P :300

Gdh 298:VPFERGLAETIEWYRDNRRAWWEPLKSAFDGGK~~~:329
 Tyla2 298:TGITEGLAGTVAWYRDNRRAWWEPLKRSFGGRELERA:333
 SgcA 298:VAFEDGLAATVKWYHENRSWWOPLKEAAGLLDAVG~:332
 MtmE 299:REFGDALAE TVA WYRHHRAWWEPLTRAYCAVAA~~~:331
 consensus 301: f egLA Tv WYrdnRaWWePLk a gg :336

Fig. 8A

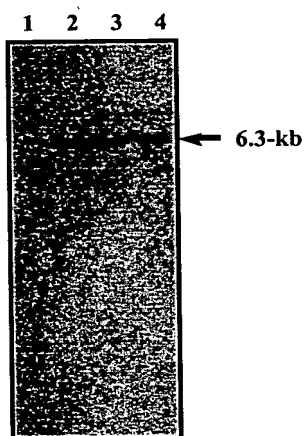
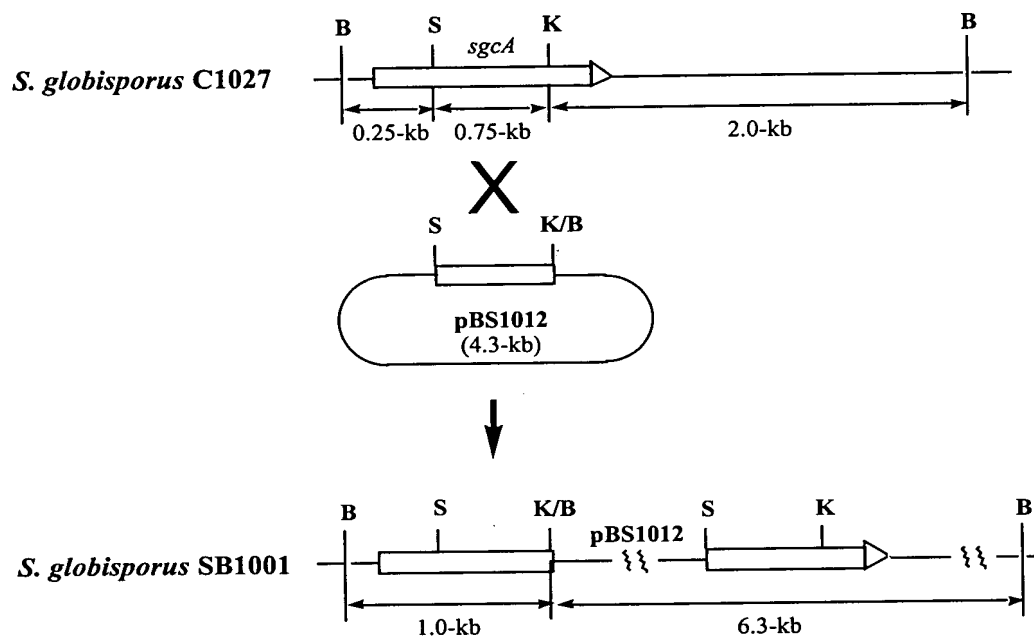


Fig. 8B

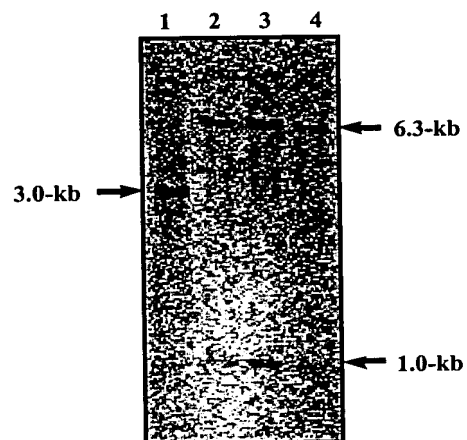


Fig. 8C

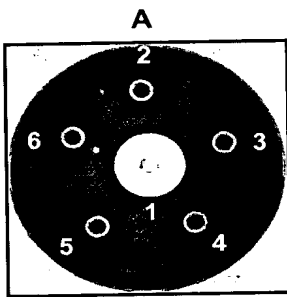


Fig. 9A

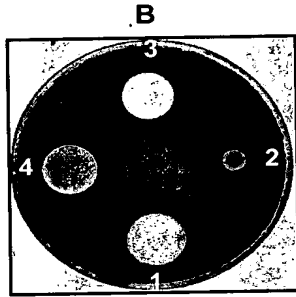


Fig. 9B

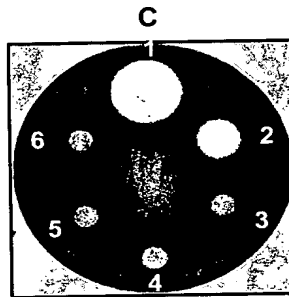


Fig. 9C

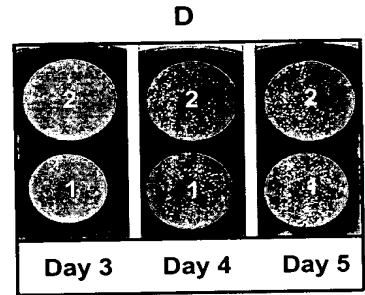


Fig. 9D